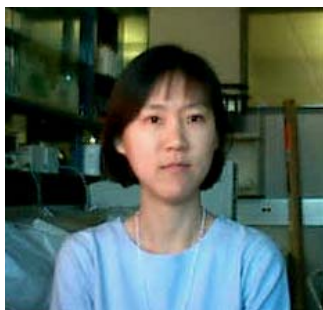




Transcriptional Regulation of the Human Manganese Superoxide Dismutase (MnSOD) Gene

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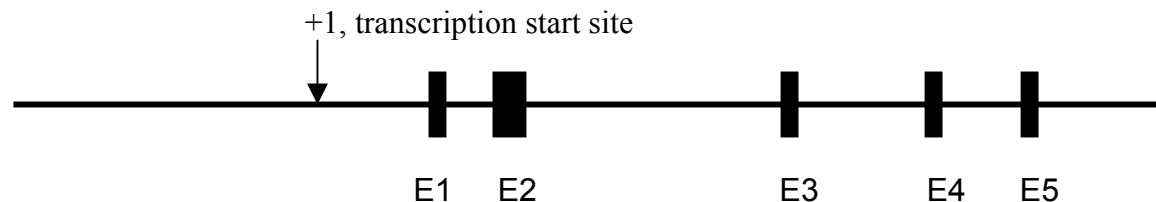
Why regulation of MnSOD is important?

- MnSOD is essential for the survival of aerobic life
- increased MnSOD level protects normal tissues against oxidative stress-mediated pathological conditions
- MnSOD suppresses neoplastic transformation, cancer phenotypes, and metastatic potential
- MnSOD alters gene expression associated with proliferation/apoptosis

(Carlioz A. and Touati D., 1986; Wong G.H. *et al.*, 1989; St. Clair D.K. *et al.*, 1992; Church S.L. *et al.*, 1993; St. Clair D.K. *et al.*, 1994; Safford S.E. *et al.*, 1994; Li Y. *et al.*, 1995; Kiningham K.K. *et al.*, 1997; Drane P. *et al.*, 2001; Zhao Y. *et al.*, 2002)

The human MnSOD gene (GenBank Accession no.S77127)

- locates on chromosome 6q25
- is a single copy gene
- consists of 5 exons and 4 introns

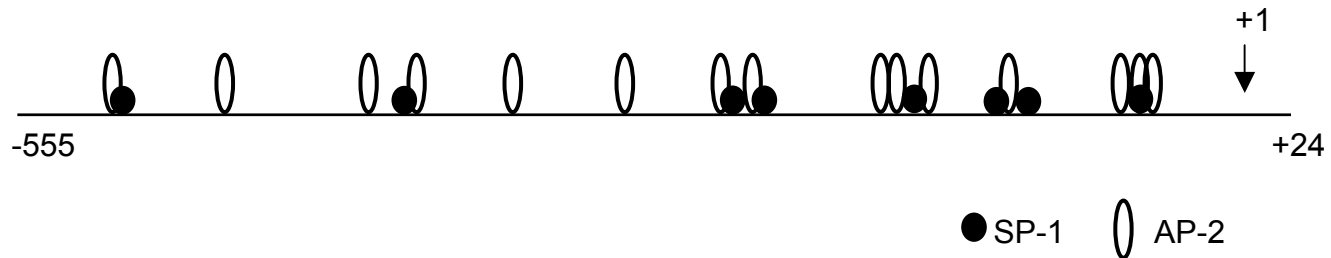


- is transcribed and processed into multiple transcripts (1, 4, and 6 kb)
- is encoded for a 222-amino acid protein containing a 24 amino acids leader peptide necessary for mitochondrial targeting

(Beck Y. *et al.*, 1988; Ho Y-S. and Crapo J.D., 1988; Wispe J.R. *et al.*, 1989; Church, S.L., 1990; Church S.L. *et al.*, 1992; Wan X.S. *et al.*, 1994)

The human MnSOD promoter

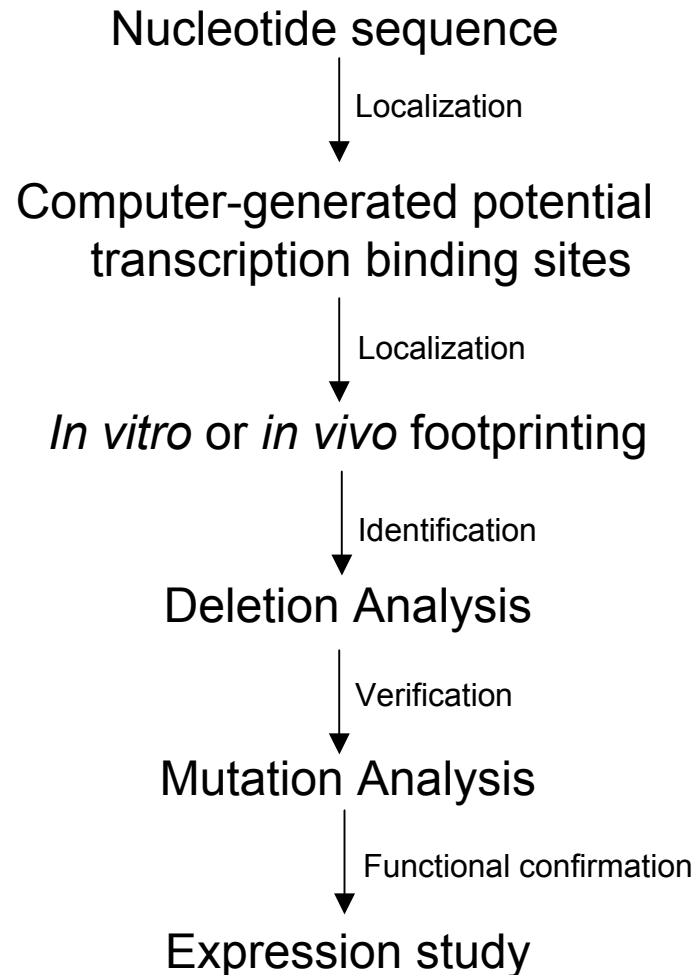
- consists of 78% GC without a TATA or CAAT box
- contains multiple SP-1 and AP-2 binding sites



- may also contain binding site for other transcription factors especially zinc finger family members such as Sp3, AML-1a, MZF1

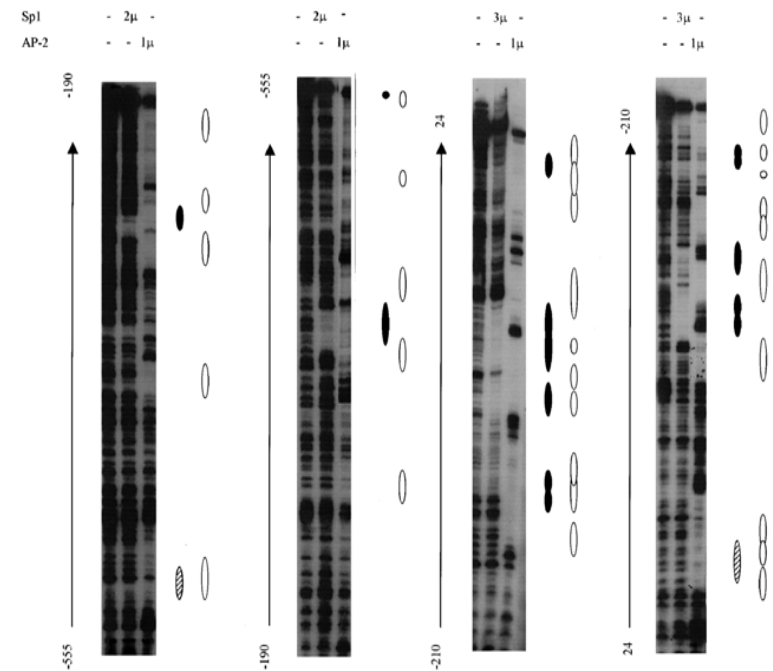
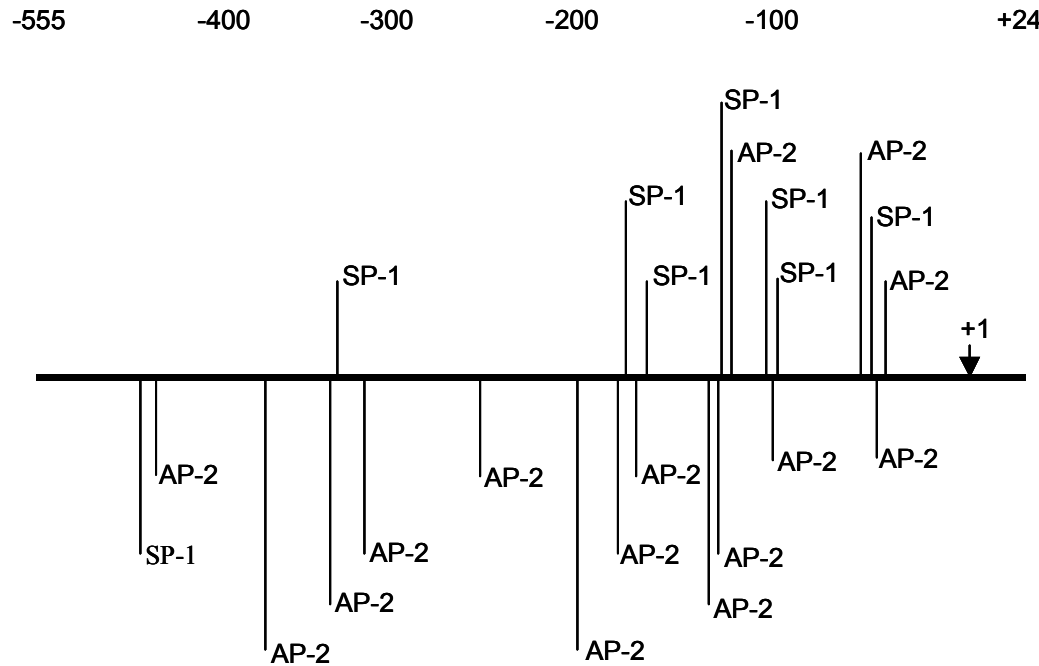
(Wan X.S. *et al.*, 1994; Yeh C-C. *et al.*, 1998)

Methods for identification of regulatory elements



Localization:

MnSOD promoter contains overlapping SP-1 and AP-2 binding sites



Computer Analysis Computer analysis depicted the potential binding sites for SP-1 and AP-2 on the MnSOD promoter region (marked on the top). *In vitro* footprinting (right) revealed additional SP-1 and AP-2 binding sites that were not identified by computer analysis (marked on the bottom).

Note: -These binding sites may not function *in vivo*.

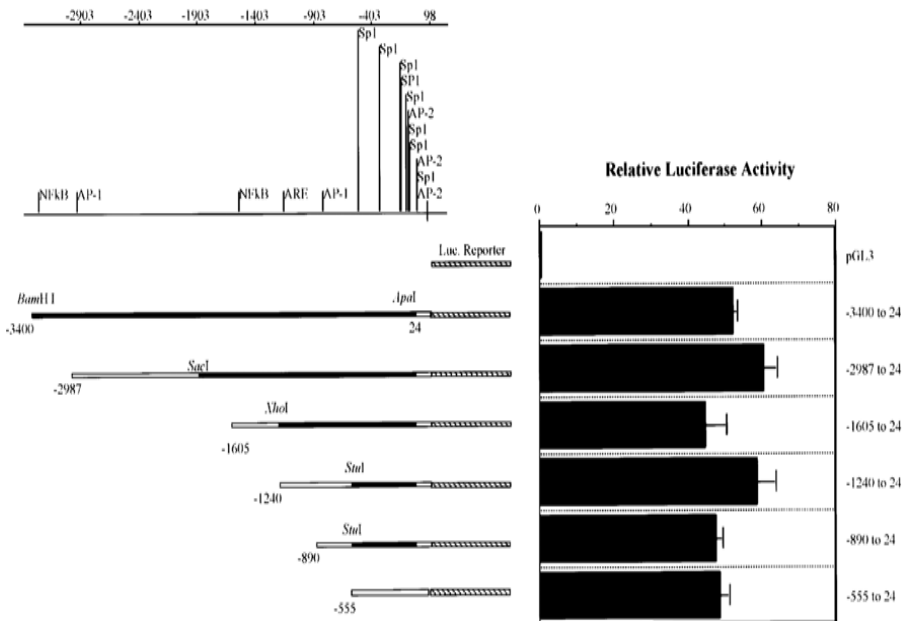
- Some functional binding sites may not be identified by computer analysis.

***In vitro* footprinting.** SP-1 and AP-2 binding sites were identified in both strand of the promoter region by DNase I digestion with purified SP-1 or AP-2 protein. The binding site for SP-1 (solid oval) and AP-2 (open oval) are shown. The shaded oval is the binding site for SP-1 that can not be detected, but can be detected on the complementary strand.

(Wan X.S. *et al.*, 1994; Xu Y. *et al.*, 2002)

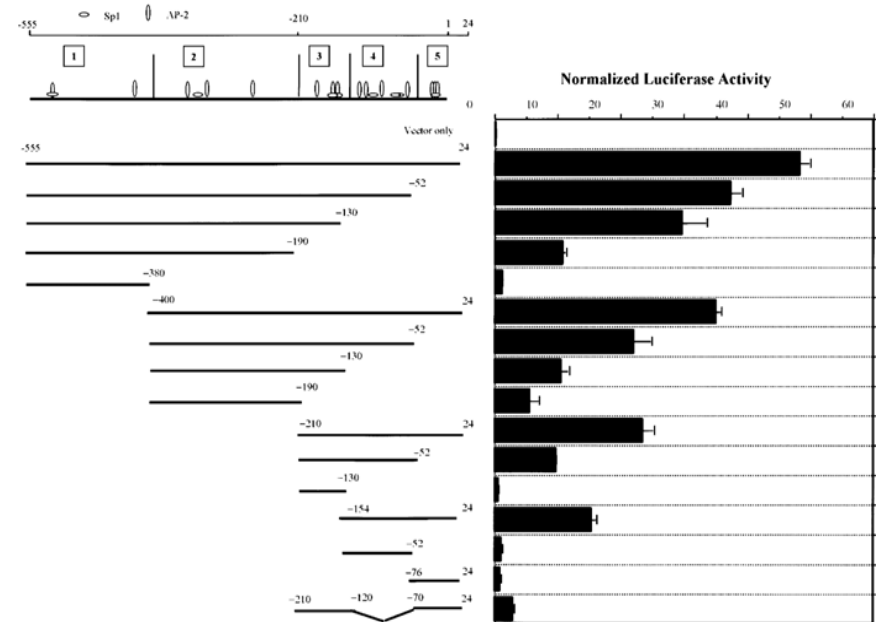
Identification:

The 5' flanking region from -555 of the transcription start site is sufficient for a high-level transcription



Deletion Analysis. Fragments containing various length of the 5' flanking region were subcloned into pGL3 to drive the expression of the reporter gene. The promoter activity of each fragment was determined by luciferase activity assay.

(Xu Y. *et al.*, 2002)

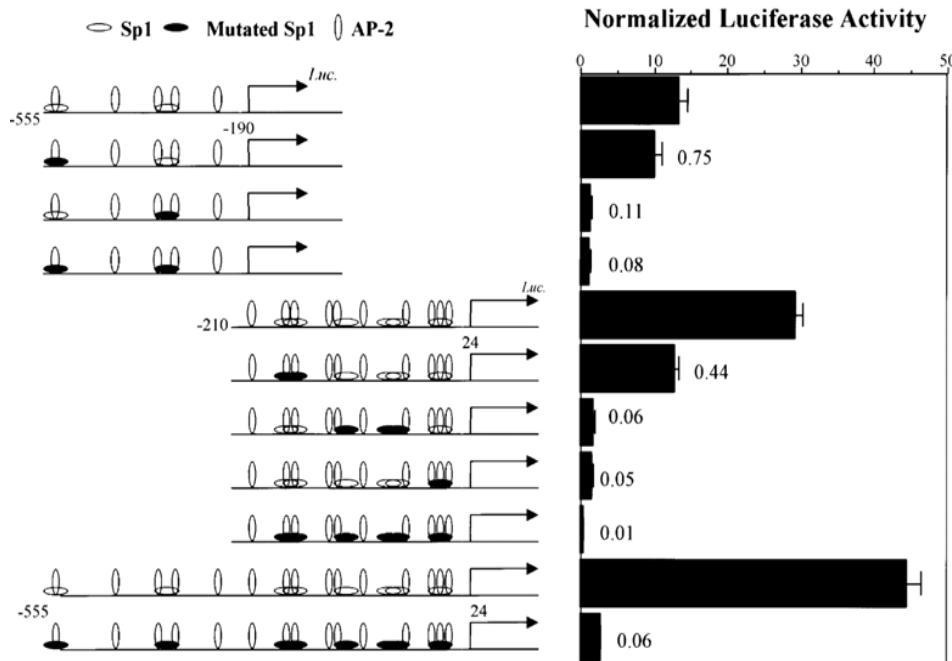


Deletion analysis. Deletion of five binding domains containing 8 SP-1 binding sites and 15 AP-2 binding sites in the five motifs are illustrated at the top. Deletion fragments were generated by PCR based on the binding motifs and then subcloned into pGL3 to drive the expression of the reporter gene.

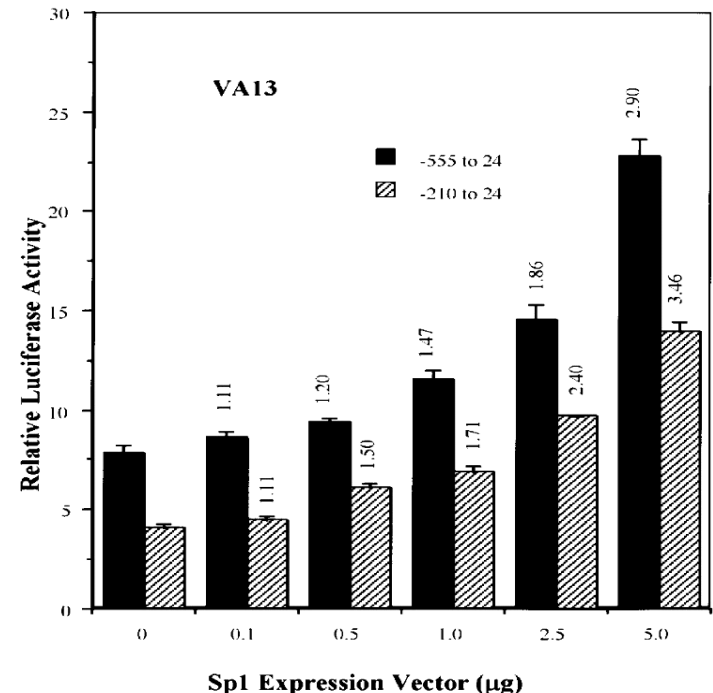
Note: - At least two binding motifs are needed for a minimal transcription.

Verification and Functional confirmation:

SP-1 plays a positive role in the constitutive transcription



Mutation Analysis. SP-1 binding sites were mutated by site-directed mutagenesis and then subcloned into pGL3 to drive the expression of the reporter gene. The role of each SP-1 binding site was determined by luciferase activity assay. The number by the error bars indicated the fold reduction from non-mutated control.

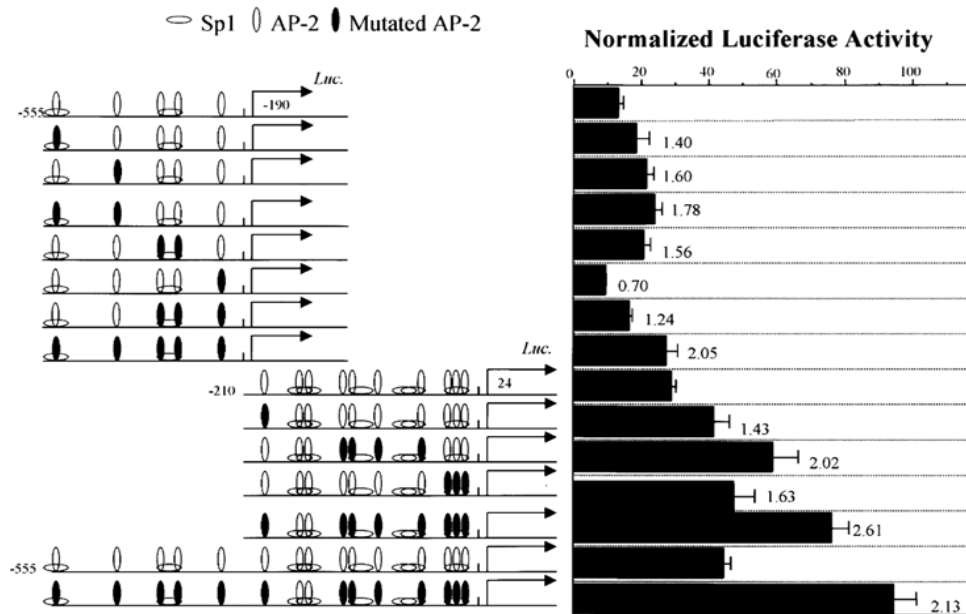


Expression study. The effect of SP-1 on the MnSOD promoter (-555 to +24 and -210 to +24). VA-13 cells were co-transfected with the promoter and various amounts of the SP-1 expression vector. The fold induction is indicated by the number above the error bars.

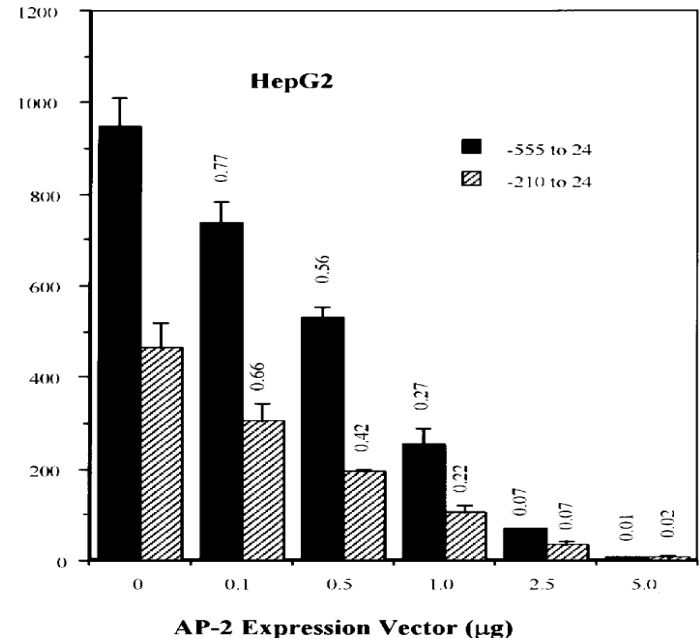
(Xu Y. *et al.*, 2002)

Verification and Functional confirmation:

AP-2 plays a negative role in the constitutive transcription



Mutation analysis. AP-2 binding sites were mutated by site-directed mutagenesis and then subcloned into pGL3 to drive the expression of the reporter gene. The role of each AP-2 binding site was determined by luciferase activity assay. The number by the error bars indicated the fold induction from non-mutated control.

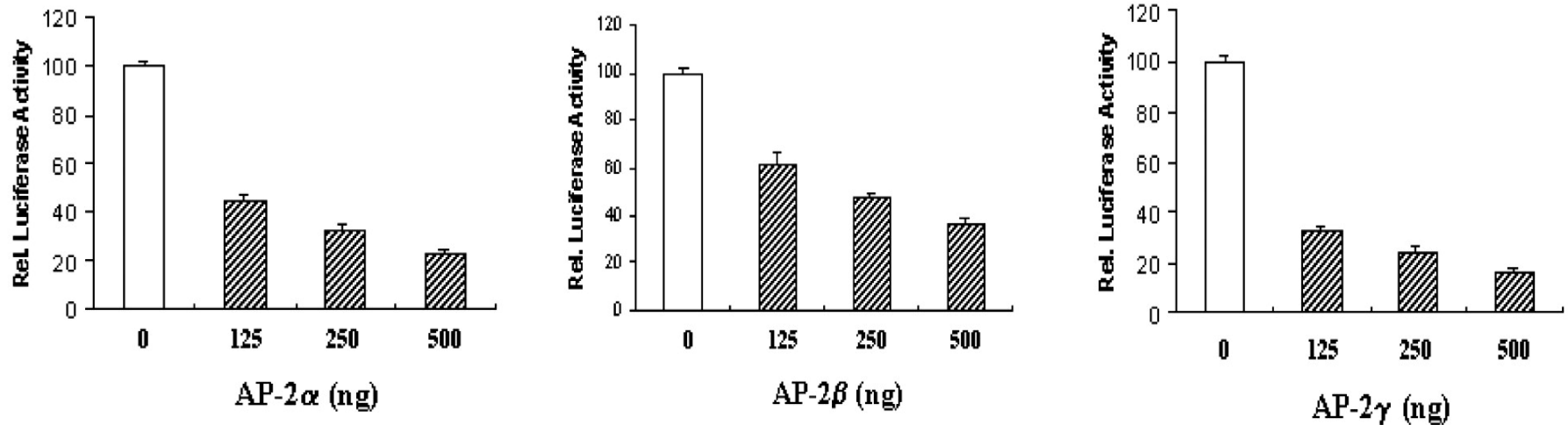


Expression study. The effect of AP-2 on the human MnSOD promoter (-555 to +24 and -210 to +24). HepG2 cells were co-transfected with the promoter and various amounts of the AP-2 expression vector. The fold reduction is indicated by the number above the error bars.

(Xu Y. *et al.*, 2002)

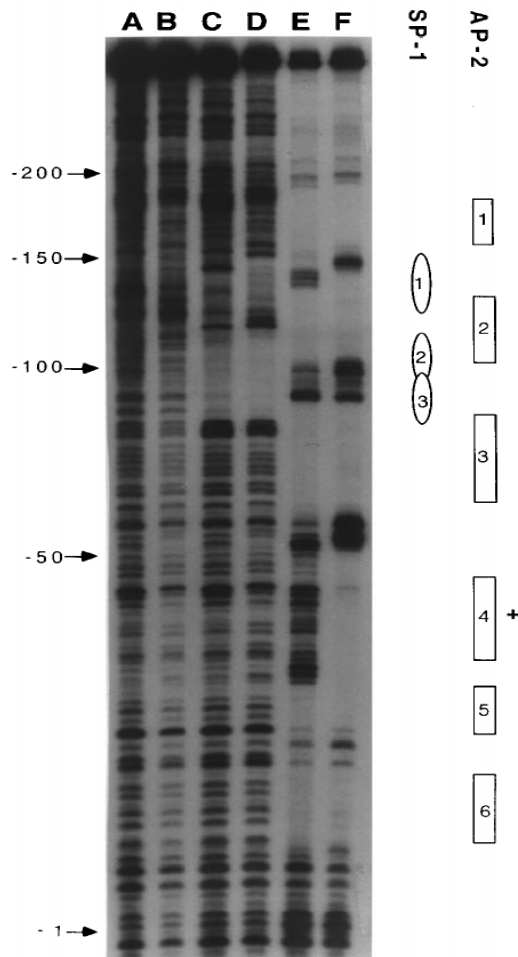
Functional confirmation:

A family of AP-2 proteins represses promoter activity



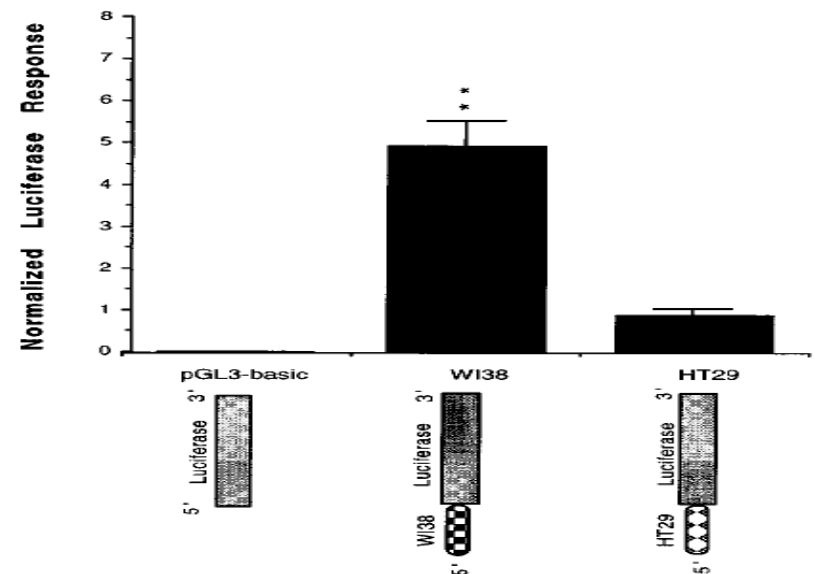
Expression study. HepG2 cells were co-transfected with MnSOD promoter (-555/+24) and three different isoforms of AP-2. The effect of each AP-2 isoform was determined by luciferase activity assay. (From Zhu C-H. *et al.*, *JBC*. 276, 2001. With permission)

Mutations in the promoter may contribute to decreased expression of the human MnSOD gene in some cancer cells



Footprinting analysis. Dnase I footprinting analysis of the human MnSOD promoter using purified SP-1 and AP-2 proteins. Normal promoter without protein (A), with SP-1 protein (C) with AP-2 protein (E); Mutated promoter without protein (B), with SP-1 protein (D), with AP-2 protein (F). The binding patterns of SP-1 and AP-2 are indicated on the right. (+) represents an additional AP-2 binding site in the mutated promoter.

Effect of mutations in the promoter on gene expression. Human fibroblast cells were transfected with pGL3 plasmids containing promoter from WI38 (normal) or mutated promoter (HT-29). The promoter activity was measured by luciferase activity assay.



(Xu Y. *et al.*, 1999)

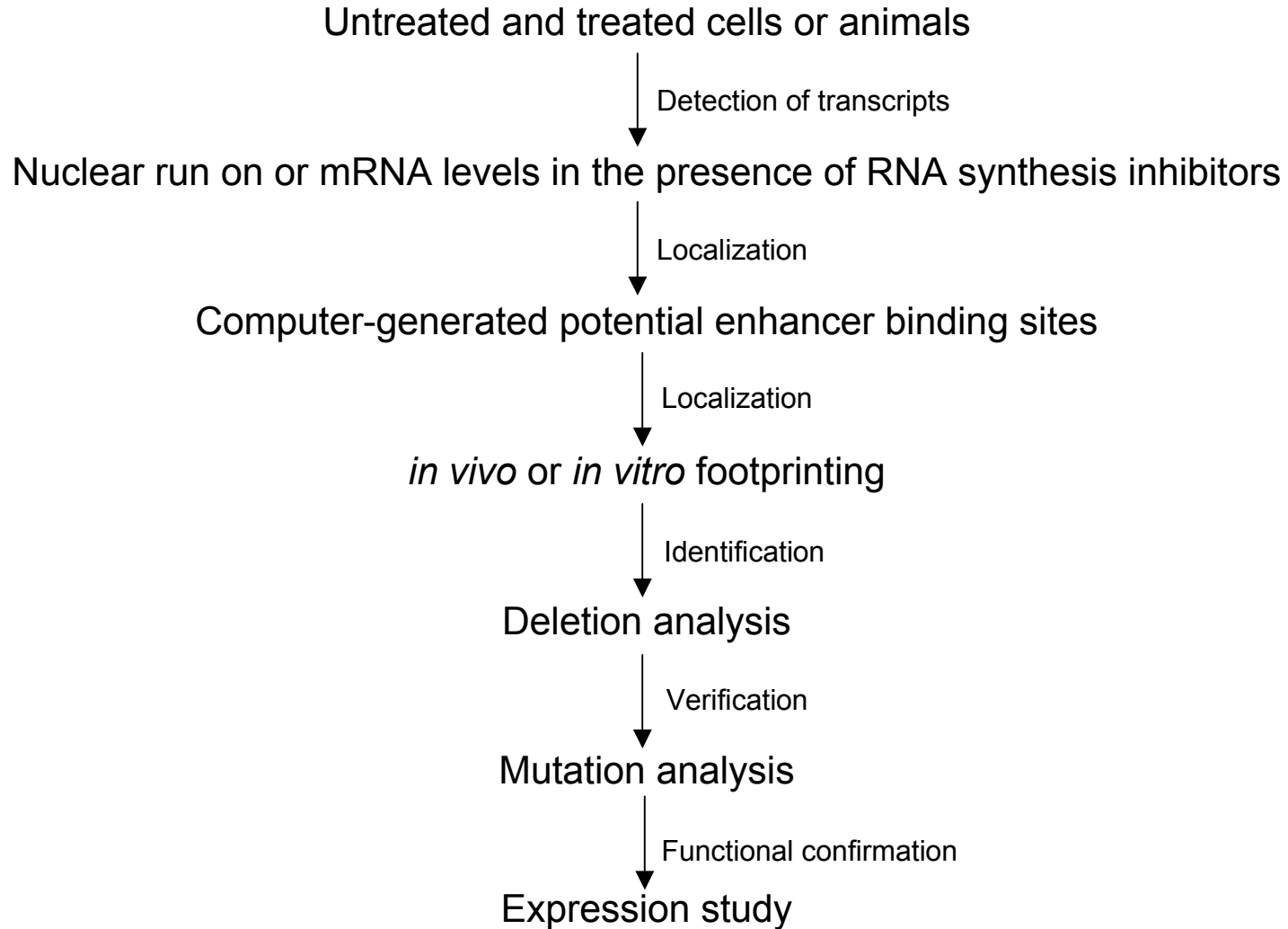
MnSOD is inducible

- MnSOD gene is highly inducible by various agents and conditions that cause oxidative stress. Enhancer elements have been identified in the 5' flanking region as well as in an intronic region of the human MnSOD gene
- Enhancer elements identified in the 5' flanking region including MnSOD TPA-responsive element (MSTRE) located between -1292 and -1202 on the 5' flanking region of the human MnSOD gene in lung carcinoma cells, and SP-1 mediated TPA-responsive elements in the GC rich region of the promoter in hepatocarcinoma cells
- Enhancer elements identified in the intronic region is located between 1741 and 2083. It contains binding sites for several transcription factors including C/EBP-1, -2, -X, NF- κ B, and NF-1

Note: The elements identified in the 5' flanking region appear to function in cell type specific manners.

(Wong G.H. and Goeddel D.V., 1988; Wong G.H. *et al.*, 1989; Visner G.A. *et al.*, 1990; Fujii J. and Taniguchi N., 1991; Xu Y. *et al.*, 1999; Kim H-P. *et al.*, 1999; Porntadavity S. *et al.*, 2001)

Methods for Identification inducible elements



Identification:

TPA-responsive element (MSTRE) located between -1292 and -1202 on the 5' flanking region of the human MnSOD gene

	pSODLUC	Relative Light Units		F.I.*
		-TPA	+TPA	
-3215 -2883 NF-KB API	LUC -3340	1.71 ± 0.28	3.18 ± 0.40	1.86
	LUC -2951	1.75 ± 0.11	2.98 ± 0.15	1.70
	LUC -2462	2.22 ± 0.14	3.82 ± 0.09	1.72
-1551 -1258 -820 NF-KB CREB API	LUC -1900	2.48 ± 0.05	4.77 ± 0.08	1.93
	LUC -1396	3.38 ± 0.13	6.97 ± 0.17	2.06
	LUC -1292	2.93 ± 0.23	8.15 ± 0.12	2.79
	LUC -1202	2.49 ± 0.11	3.38 ± 0.28	1.36
	LUC -1103	2.26 ± 0.21	3.37 ± 0.31	1.49
	LUC -1058	3.71 ± 0.32	3.58 ± 0.00	0.96
	LUC -744	3.52 ± 0.09	4.29 ± 0.19	1.22
	LUC -451	2.82 ± 0.20	3.57 ± 0.08	1.27
	LUC -262	1.56 ± 0.18	2.12 ± 0.13	1.36
	LUC -106	0.71 ± 0.04	0.72 ± 0.07	1.02
	LUC -1	0.26 ± 0.02	0.33 ± 0.01	1.25

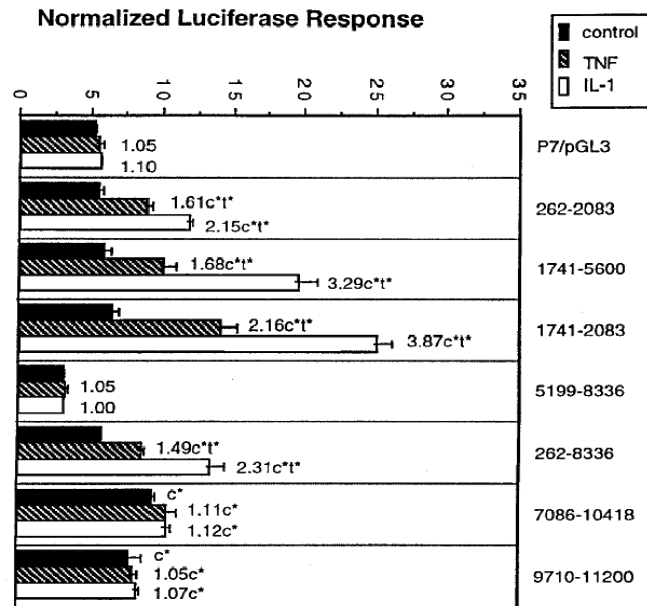
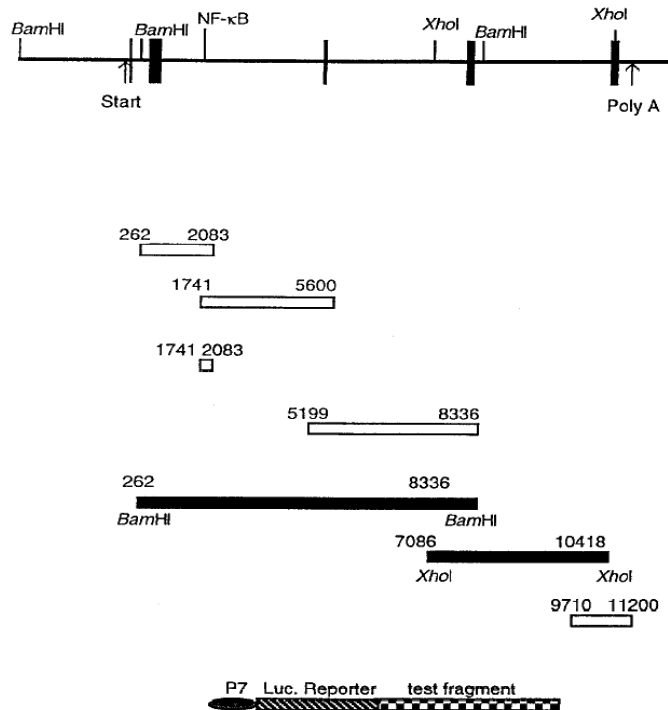
*F.I. = Fold Induction

Deletion analysis. Fragments of 5' flanking region were subcloned into pGL3 to drive the expression of the reporter gene. The promoter activity of each fragment was measured by luciferase activity assay. The fold induction is indicated by the number in the last column.

(From Kim H-P. *et al.*, JBC 274, 1999. With permission.)

Identification:

A region between 1741 and 2083 in intron 2 is sufficient for the induction of the human MnSOD gene by TNF and IL-1.

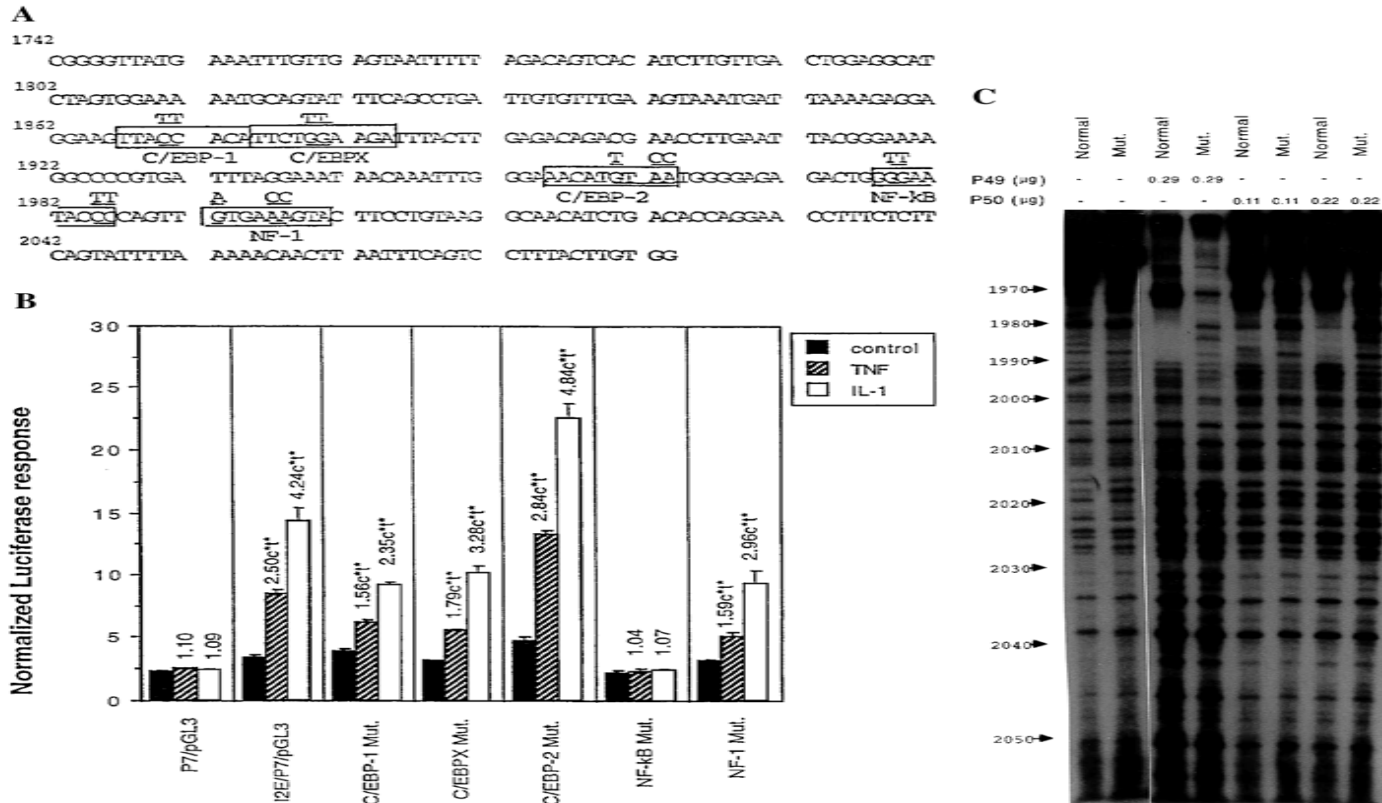


Deletion analysis. Fragments of the MnSOD gene were generated by restriction digestion (solid box) or PCR (open box) and then subcloned downstream of the reporter gene (pGL3) driven by the promoter (P7). The enhancer capability of each fragment was determined by luciferase activity assay. The number by the error bars indicate the fold induction compare to untreated cells. t*, significant differences between treatment and nontreatment using the same construct ($p \leq 0.01$). c*, significant differences between the constructs and the vector control (P7/pGL3) receiving the same treatment ($p \leq 0.01$).

(Xu Y. *et al.*, 1999)

Verification:

An intronic enhancer contains NF- κ B binding site responsible for MnSOD induction



Mutation analysis. (A) The binding site for transcription factors in the intronic enhancer are boxed. The mutated bases change are on the top. (B) The role of each binding site was determined by luciferase activity assay. The number by the error bars indicate the fold induction. (C) Footprinting analysis of the NF- κ B binding site in the I2E fragment using purified p49 or p50 proteins. The NF- κ B binding site is marked on the right.

(Xu Y. *et al.*, 1999)

Conclusions about the human MnSOD gene:

- is a single copy gene located on chromosome 6q25
- The promoter region contains multiple SP-1 and AP-2 binding sites
- SP-1 plays a positive role in the transcription of the gene
- AP-2 plays a negative role in the transcription of the gene
- is highly inducible by various agents and conditions
- Enhancer elements are located in the 5' flanking region as well as in an intronic region

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